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OM protein - protein search, using sw model

Run on: May 17, 2002, 23:39:26 ; Search time 145.84 Seconds
(without alignments)
274.181 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846

Sequence: 1 MEPPKQKQVEFDYDGERLG.....TEEDIRAKKALHPRRSSTS 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq_032802:*

1: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:**

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3: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:**

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8: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:**

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16: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:**

17: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:**

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19: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:**

20: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:**

21: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:**

22: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1846	100.0	360	21	AAV44674	Human DAP-kinase-r
2	1717	93.0	359	22	ABG09274	Novel human diapo
3	1248	67.6	1423	16	AAW74205	Human death associ
4	1248	67.6	1423	19	AAW71367	Death associated p
5	1166	63.2	454	20	AAW06921	Human ZIP-kinase (
6	1166	63.2	454	22	AAW93338	Human polypeptide,
7	1162	62.9	454	22	AAW94378	Human protein sequ
8	1162	62.9	454	22	AAW67425	Amino acid sequenc
9	1140	61.8	448	20	AAW06922	Murine ZIP-kinase
10	761	41.2	160	21	AAW84323	A human cardiovasc
11	668.5	36.2	414	20	AAV27161	Human DRAK1 protei

12	668.5	36.2	414	22	ABW56525	Novel protein kina
13	660	35.8	7107	22	ABW58144	Drosophila melanog
14	654	35.4	260	20	AAV43924	Chicken protein ki
15	649.5	35.2	372	22	ABW56524	Novel protein kina
16	641.5	34.8	372	20	AAV27162	Human DRAK2 protei
17	641.5	34.8	372	22	ABW56523	Novel protein kina
18	641	34.7	814	22	ABW56534	Novel protein kina
19	641	34.7	814	20	AAV42111	Human ischaemic he
20	639.5	34.6	839	21	ABW56864	Human prostate can
21	633.5	34.3	291	22	ABW5502	Human protein kina
22	627	34.0	413	22	ABW56522	Human protein kina
23	603.5	32.7	612	22	AAU03521	Human protein kina
24	593.5	32.2	596	22	AAW7544	Amino acid sequenc
25	591	32.0	913	22	ABW62810	Drosophila melanog
26	591	32.0	913	22	ABW65968	Drosophila melanog
27	581	31.5	1289	20	AAV27163	Peptide Seg ID No:
28	581	31.5	1289	21	AAV56781	Human Trid protein
29	580.5	31.4	450	22	ABG08502	Novel human diapo
30	571.5	31.0	261	20	AAV43923	Rabbit protein kin
31	565.5	30.6	356	22	ABW84360	Amino acid sequenc
32	564.5	30.6	307	18	AAW34882	Novel human phosph
33	564.5	30.6	307	20	AAW76803	Human phosphorilas
34	564.5	30.6	307	21	AAV52303	Novel human phosph
35	564	30.6	355	22	AAE11777	Human kinase (PKIN
36	564	30.6	355	22	AAW41268	Human polypeptide
37	564	30.6	357	22	AAE11768	Human kinase (PKIN
38	564	30.6	385	22	AAW39482	Human polypeptide
39	564	30.6	385	22	AAW84359	Amino acid sequenc
40	562	30.4	357	22	AAU03508	Human protein kina
41	556	30.1	355	22	ABW50055	Murine Dendritic C
42	546	29.6	343	22	AAU03511	Human protein kina
43	545	29.5	358	19	AAW50159	Calmodulin-depende
44	543.5	29.4	497	22	AAW41517	Human polypeptide
45	541	29.3	26926	22	AAU03536	Human titin (conn

ALIGNMENTS

RESULT	1	
AAV44674	AAV44674 standard; Protein: 360 AA.	
ID	AAV44674:	
AC	AAV44674:	
XX	18-APR-2000 (first entry)	
DT	Human DAP-kinase-related protein 1 (DRP-1).	
DE		
XX	DAP-kinase-related protein 1; DRP-1; Death-Associated Protein;	
KW	calmodulin-dependent serine/threonine kinase; apoptosis; dimerisation;	
KW	cytostatic; antiproliferative; immunosuppressive; metastasis; human;	
KW	treatment; cancer; psoriasis; autoimmune disease; screening.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Domain	13..275
FT	Domain	/label= Serine/Threonine_kinase_domain
FT	Domain	292..320
FT	Domain	/label= Calmodulin_regulatory_domain
FT	Region	321..360
FT		/label= C-terminal_region
FT		/note= Critical for DRP-1 dimerisation and apoptotic induction
XX	WO966030-A1.	
PD	23-DEC-1999.	
XX		
XX	15-JUN-1999: 99WO-US13411.	
PF		
XX	15-JUN-1998: 98US-0089294.	

XX (YEDA) YEDA RES & DEV CO LTD.
PA (MCIN/) MCINNIS P A.
XX
XX Kimchi A:
XX WPI: 2000-147148/13.
DR N-PSDB; AAZ49765.
XX
PT Calmodulin-dependent serine/threonine kinase capable of inducing
PT apoptosis used in the treatment of e.g. cancer -
PS
PS Claim 1; Fig 1; 67pp; English.
XX
CC The present sequence is DAP (death-associated protein)-kinase-related
CC protein 1 (DRP-1), which is a calmodulin-dependent serine/threonine
CC kinase. DRP-1 is a cytoplasmic protein capable of inducing apoptosis
CC by dimerisation. It shows significant homology to DAP kinase. It has
CC cytosolic, antiproliferative and immunosuppressive activity and can be
CC used for inhibiting growth/metastasis of tumours and promoting
CC death of tumour cells. It can also be used in the treatment of cancer,
CC psoriasis and autoimmune diseases. Fragments of DRP-1 DNA are useful as
CC probes for screening individuals with a predisposition to cancer.
XX
SQ Sequence 360 AA;
XX
Query Match 100.0%; Score 1846; DB 21; Length 360;
Best Local Similarity 100.0%; Pred. No. 6,1e-153;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPRKQKVEDFYIGEELSGQFAIVKCKREKSTGLEVAAKFIKRSRGRGSRREE 60
Db 1 mepfqgqvdeftdgelsgqfaiivkckreksstglevaaakfkkrgsrgrsvree 60
QY 61 IEREYSILROYLHNHNVITLHVNRYENKRDVYHILEVSGGELFDPLAQKESLSEEAATSTFI 120
Db 61 IEREYSILROYLHNHNVITLHVNRYENKRDVYHILEVSGGELFDPLAQKESLSEEAATSTFI 120
QY 121 KQILDGVNVLKTRKKAHEDLKPENIMLDKNIPPHIKLIDFGLAHEIEDGVEFNINFT 180
Db 121 KQILDGVNVLKTRKKAHEDLKPENIMLDKNIPPHIKLIDFGLAHEIEDGVEFNINFT 180
QY 181 PEFAPEIYNVEPLGLEADMSIGVITYILSGASPLGDTKQETLANITSVYDDEEF 240
Db 181 PEFAPEIYNVEPLGLEADMSIGVITYILSGASPLGDTKQETLANITSVYDDEEF 240
QY 241 FSHSELAKEDEIRKILVETREKRLTIQALRHPWITTPVDNOQAMWRRESVNLERNKQY 300
Db 241 FSHSELAKEDEIRKILVETREKRLTIQALRHPWITTPVDNOQAMWRRESVNLERNKQY 300
QY 301 VRRMKLSFSIVSLCNHLTRSLMKVHLRPDEDLNCSDETEEDJARRKALHPRRSST 360
Db 301 VRRMKLSFSIVSLCNHLTRSLMKVHLRPDEDLNCSDETEEDJARRKALHPRRSST 360
RESULT 2
ABG09274
ID ABG09274 standard; Protein: 359 AA.
XX
AC ABG09274;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #9265.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
XX

PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX WPI: 2001-639362/73.
DR N-PSDB; AAS73461.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
PS
PS Claim 20; SEQ ID No 39633; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 359 AA;
XX
Query Match 93.0%; Score 1717; DB 22; Length 359;
Best Local Similarity 99.1%; Pred. No. 1.1e-141;
Matches 337; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 21 SQQFAIVKCKREKSTGLEVAAKFIKRSRGRGSRREEIREVSIROYLHNHNVITLH 80
Db 20 sqgfaiivkckreksstglevaaakfkkrgsrgrsvreeirevsiroylhnvltlh 79
QY 81 DYENKRDVYHILEVSGGELFDPLAQKESLSEEAATSTFIKQILDGVNVLKTRKKAHED 140
Db 80 dyenrtdvylhilevsggeldfdlqkessleeaatsfikqildgvnvlhkkkiahfcl 139
QY 141 KPEINIMLDKNIPPHIKLIDFGLAHEIEDGVEFNINFTPEFAPEIYNVEPLGLEADM 200
Db 140 kpenimldknipphiklidgeaheliedgvefninftpefapeiynveplgleadm 199
QY 201 WSIGVITYILSGASPLGDTKQETLANITSVYDDEEFSSHSELAKEDEIRKILVET 260
Db 200 wsigvityilsgasplfgdtkqetlanitavsydddeeffshtselakdfirklivket 259
QY 261 KKRRLTIQALRHPWITTPVDNOQAMWRRESVNLERNKQYVRRMKLSFSIVSLCNHLTR 320
Db 260 krrlidgealrhpwiltppvdnqamwrrsvnlernkqyvrrmklsfslvslcnhltr 319
QY 321 SLMKVHLRPDEDLNCSDETEEDJARRKALHPRRSST 360
Db 320 slmkkvhlrpdedlncsdteedjarrkahlprrrsst 359

Query	Sequence	1423 AA:
Query Match	67.6%; Score 1248; DB 16; Length 1423;	
Best Local Similarity	66.5%; Pred. No. 6.1e-100;	
Matches	236; Conservative 60; Mismatches 43; Indels 16; Gaps 3;	
QY	1 MEPRKQKQVEDFDYDGEELSGGQFAIVKCKREKSTGLEAYAKFKRKROSRSRSGVSRBE 60	
DB	1 mtvfignvdvdydtgeelsgqfayvkkckreksltgltpkpfllkrtktsrrgvsred 60	
QY	61 IEREVSILROVLHNVTLLHDVYENKRPDVVHILEVSGGELFDPLAOKRESISEEATSF 120	
DB	61 IEREVSILKEQHPNVTLLHVEYENKSTVLLILEVAGGELFDPLAEKESILEEATEFL 120	
QY	121 KQILDVNVYLLTKTKLAHEDLKREPMMLDKNKIPRIKILDFGLAHEIEDGEVEFNKFGT 180	
DB	121 KQILDVNVYLLTKTKLAHEDLKREPMMLDKNKIPRIKILDFGLAHEIEDGEVEFNKFGT 180	
QY	181 PEFAPELVNTEPLGLEADWMSIGVITYILLSGASPLGDTKQETLANITSVSYDFDEEF 240	
DB	173 pefapeelvnyepjgleadwmsigvityillsgasplfgdtkqetlanisvnyfedef 232	
QY	241 FSHRSELAQDFTRKILVKEVTRKRLTIQDALNHPVTPVDNQOAMVRSSVNLNENFRQY 300	
DB	233 fshselaqlakdftrllvdkpkrmltqgsldhnpwtkpdktdqalsrksavvmekfkfa 292	
QY	301 VRRRWKLSFSLVSCNHLTRSLMKKVHL--RPDEDLNCGSDPFEEDLARRKALH 352	
DB	293 arkkwkgvrrllslcqrslrslfslrsmvsarsddtl-----deedsfvmkailn 342	
RESULT	4	
AAW71367		
ID	AAW71367 standard; Protein: 1423 AA.	
XX	AAW71367;	
XX		
DT	12-JAN-1999 (first entry)	
DE	Death associated protein-2 (DAP-1, DAP-kinase).	
KW	Death associated protein; DAP-2; cell death; tumour cell; DAP-kinase;	
KW	metastatic activity; cancer; psoriasis; autoimmune disease;	
KW	programmed cell death; degenerative neurological disease;	
KW	Alzheimer's.	

OS Homo sapiens.
XX PN WO9839429-A2.
XX PD 11-SEP-1998.
XX PF 03-MAR-1998; 98WO-IL00102.
XX PR 03-MAR-1997; 97US-0810712.
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX PI kimchi A;
XX DR WPI: 1998-520781/44.
XX N-PSDB; AAY60289.
PT New isolated death associated protein nucleic acids - used for the
PT diagnosis and treatment of disorders associated with programmed cell
PT death, e.g. cancers, autoimmune disease or neurological disease
XX
XX PS Disclosure; Fig 8; 157pp; English.
XX
XX CC The present sequence represents a death associated protein-2 (DAP-2,
XX CC DAP-kinase). The DAP genes and proteins are used for promoting death of
XX CC normal or tumour cells, and for suppressing the metastatic activity of
XX CC tumour cells. They can be used in the treatment of diseases or disorders
XX CC associated with uncontrolled pathological growth, e.g. cancer,
XX CC psoriasis, autoimmune diseases and others. Agents which antagonise,
XX CC inhibit or neutralize DAP products are used for protecting cells from
XX CC programmed cell death. In this case they can be used for the treatment
XX CC of degenerative neurological diseases, e.g. Alzheimer's, prevention of
XX CC death of T cells in AIDS patients, prevention of rejection associated
XX CC cell death in transplants, and protection of normal cells from
XX CC the cytotoxic effects of anti-cancer therapies.
XX
XX SQ Sequence 1423 AA;

Query Match 67.6%; Score 1248; DB 19; Length 1423;
Best Local Similarity 66.5%; Pred. No. 6.1e-100;
Matches 236; Conservative 60; Mismatches 43; Indels 16; Gaps 3;

QY 1 MEPEKQKVEDFDIGELSGGOFATVKKCREKSTGLEVAKFTKRQSRASRGVSRRE 60
DB 1 mvtfgenvdyydtgeelsgqfatavkkcrekstgldypakfllkrrtkssrrgvared 60
QY 61 IEREVSILROYLHNHNTTLHDVYENRRTDVVHILEVSGGELFDFLAQKESSEBEATSFI 120
DB 61 Ierevsilkeiqhpnvltlhevnyenktvlllelvaggeifdfiaekeslteeaatefi 120
QY 121 KQILDGVNVLHTKKIAHFDLKPENIMLDKNIPPIHKLIDFGLAHIEDGVEFEKNIFGT 180
DB 121 kqilngvnyllhstqldandlkrpenimldtrvnpkrriklidlft-----gnefkni fgt 172
QY 181 PEVVAPEIVNTEPLGLADMMISGIVITYILLSGASPLFGDTKOETLANITSVSDPEEF 240
DB 173 pefvapeivnyepgladmmisgivytlilsgasplfgdtkgeclanvaavnyedeey 232
QY 241 FSHSTELAKDFIRKLVKETRKRLLTIOEALRHPWITPVNDQAMVRESVNLNENFRKQY 300
DB 233 fshstelsakdfirrllykvpdkrrmtlqdsiqhpkpdkcgalrskaavnmekffkfa 292
QY 301 VRRRMKLSFSIVSLCNHLTRSLMKKVVHLPDE--DLRNCESDTEEDIAARRKALH 352
DB 293 arrkwwkgsvrlisicqlstfsflstrmsvardsdtl-----deedsfvmkaih 342

RESULT 5
AAY06921
ID AAY06921 standard; protein; 454 AA.
XX
AC AAY06921;

XX
XX DT 01-JUL-1999 (first entry)
XX DE Human ZIP-kinase (serine/threonine kinase).
XX DE
XX KW zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
XX KW leucine zipper domain; transcription factor ATR4; gene therapy; cancer;
XX KW human; murine.
XX
XX OS Homo sapiens.
XX PN EP911408-A2.
XX PD 28-APR-1999.
XX PF 24-SEP-1998; 98EP-0307747.
XX PR 26-SEP-1997; 97JP-0261589.
XX PA (NTSC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX PI Akira S, Kawai T;
XX DR WPI: 1999-246420/21.
XX N-PSDB; AAX34656.
PT New Recombinant zipper Interacting Protein Kinase (ZIP-kinase)
PT protein and DNA, useful as anticancer agents
XX
XX PS Claim 1; Page 15-18; 33pp; English.
XX
XX CC The invention provides human and murine recombinant zipper Interacting
XX CC Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine
XX CC kinases which bind the leucine zipper domain of transcription factor
XX CC ATR4. Host cells containing vectors comprising the ZIP-kinase nucleic
XX CC acids are used for the recombinant expression of the proteins. ZIP-kinase
XX CC protein and DNA are useful as gene therapeutic agents against cancer, and
XX CC as anti-cancer agents. The present sequence represents a human ZIP kinase
XX CC protein.
XX
XX SQ Sequence 454 AA;

Query Match 63.2%; Score 1166; DB 20; Length 454;
Best Local Similarity 64.7%; Pred. No. 1.9e-93;
Matches 233; Conservative 49; Mismatches 60; Indels 18; Gaps 3;

QY 1 MEPEKQKVEDFDIGELSGGOFATVKKCREKSTGLEVAKFTKRQSRASRGVSRRE 60
DB 1 mstrfgedvedhyemgeelsgqfatavrkcrqkytgyeakfllkrrlssrrgvaree 60
QY 61 IEREVSILROYLHNHNTTLHDVYENRRTDVVHILEVSGGELFDFLAQKESSEBEATSFI 120
DB 61 Ierevnlleirtrpnltlndifenkcdvlllelvaggeifdfiaekeslteeaatqfl 120
QY 121 KQILDGVNVLHTKKIAHFDLKPENIMLDKNIPPIHKLIDFGLAHIEDGVEFEKNIFGT 180
DB 121 kqilldgvhyhsrkrlahfalkpenimldknvnprikldlftglahleegnefkni fgt 180
QY 181 PEVVAPEIVNTEPLGLADMMISGIVITYILLSGASPLFGDTKOETLANITSVSDPEEF 240
DB 181 pefvapeivnyepgladmmisgivytlilsgasplfgdtkgecltnsaavnyddeey 240
QY 241 FSHSTELAKDFIRKLVKETRKRLLTIOEALRHPWITPVNDQAMVRESVNLNENFRKQY 300
DB 241 fshstelsakdfirrllykvpdkrrmtlqdslehwl-----kalltrnygedsgyrkpe 293
QY 301 VRRRMKLSFSIVSLCNHLTRSLMKKVVHLPDE--DLRNCESDTEEDIAARRKALH 357
DB 294 rrrlktlrrlkeyfiksks-----lppnsyadferfskylleaaaaaegllrelqrs 345

RESULT 6

AAM9338
 ID AAM9338 standard; Protein; 454 AA.
 XX
 AC AAM9338:
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 2875.
 XX
 KM Human: full length cDNA; cDNA synthesis; oligo-capping.
 XX
 OS Homo sapiens.
 XX
 PN EP130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI; 2001-524255/58.
 DR N-PSDB; AAK94258.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 8; SEQ ID NO 2875; 1380bp + sequence listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a polypeptide
 CC encoded by a full length human cDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 CC
 SO Sequence 454 AA:
 Query Match 63.2%; Score 1166; DB 22; Length 454;
 Best Local Similarity 64.7%; Pred. No. 1.9e-93;
 Matches 233; Conservative 49; Mismatches 60; Indels 18; Gaps 3;
 QY 1 MEPPKQKQVEDFDIGELSGCPATVKKCKREKSTGLEVAKFKKQSRASRRGVRREE 60
 DB 1 mstrdgedvedhyemgeelsgqfalyrcrkqkygkayakfkikrrlssrsrvaree 60
 QY 1 IEREVSLROVLLHNNTTLDVYENRTDVYHLELVSGGELDFDLAKESLSSEEARSTFI 120
 DB 61 lerevnlletrhpnlitlndifenkcdvyllelvsggelfdlakessldeeaqfll 120
 QY 121 KQILDGVNVLHTKRIAHFDKLPENIMLDKNIPRIHAKLIDFGLAHEDGVEPKNTFGT 180
 DB 121 kqildgvyhyskrlahfdlkpenimldknpvprlklidfglahklsagnekntfgt 180
 QY 181 PERFAPRIVNVEPLGLADAMWSIGVITYILLSGASPLGDTKOTKTLANTISVSDPEDEF 240
 DB 181 petvapeivnvepgleadamsigvityillsgaspligetkeltcnlsavnydfidey 240
 QY 241 FSHTSELAKDFIRKLIVKETRRKRLTIQELRHPWITPVNDQNAVRESVNLNPFKQY 300

Db 241 fshtselakdfirrlivkdpkrrmtlsgslshsvl-----kairrnvrgedsqtkpe 293
 QY 301 VRRRWKLSFSIVSLCNHLTRSLMKKVLHRLPE---DLRNCSDTEEDIAARKALHPRRS 357
 Db 294 rrrlkrtrikelytkshs-----lppnsyadferfiskvleaaaaeqlreldrs 345
 RESULT 7
 ID AAB94378 standard; Protein; 454 AA.
 XX
 AC AAB94378:
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:14926.
 XX
 KM Human: primer; detection; diagnosis; antisense therapy; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 14926; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 CC
 SO Sequence 454 AA:
 QY

Query Match 62.9%; Score 1162; DB 22; Length 454;
 Best Local Similarity 64.4%; Pred. No. 4.3e-93;
 Matches 232; Conservative 49; Mismatches 61; Indels 18; Gaps 3;

1 MEPEKQKVEDFYDIDGELSGQFAIVKCKRSTGLTYAAKFIKKRSRARSRCVSRRE 60
 1 mstfrqevdyemgeelsgqfaiivkckrqgkygkeyaakfkkrrlssrrgvsree 60

61 IEREVSIKQVLYHNVTLDHYENRTDVVHILELVSGELFDPFLAQKESLEBEATSPFI 120
 61 Ierevnlirelhpnlitldhdfenktvdllelvsgelldflaekesldeeatqfl 120

121 KQILDGVNVLHTKRIAHFDLKPENIMLDKNIPPIHKLIDFGLAHEIEDGVFNKIFGT 180
 121 kqildgvnylhskriahfdlkipenimldknpnprikliidfglahkieagnefnkifgt 180

181 PEFAVAPEIVNPEPLGLEADMSIGVITYTLLSGASPFGLDQKOEFLANTSVSYDFDEEF 240
 181 pefavapeivnpeplgleadmsigvitytllsgaspfglgelqetclnlsavnydfdeey 240

241 FSHTSELAKDFIRKLIVKETERKRLTIOELRHPWITPVNDQOAWVRRESVNLLENFRKOY 300
 241 fshtselakdfirklivketerkrltioelrhpwittpvndqoawvrresvnlennfrkoy 300

241 fsntgelakdfirllivkdpkrmtlsglseshwl-----kallrrnnvgedsgtkrpe 293

301 VRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDE---DLRNCESDTEEDTARRKALHPRRRS 357
 301 vrrrwklsfslvslcnhltrslmkkvhlrpde---dlrncesdteedtarrkalphrrrs 357

294 rrrlktlrkeytlkskshs-----lppnnsyadferfakvleaaaaeeglrelqrs 345

RESULT 8
 AAG67425
 ID AAG67425 standard; Protein: 454 AA.
 AC AAG67425;
 DT 26-NOV-2001 (first entry)
 DE Amino acid sequence of a human protein kinase/protein phosphatase.
 KW Human; protein kinase; protein phosphatase; signal transduction;
 KM Intracellular signalling pathway.
 OS Homo sapiens.
 PN W0200109345-A1.
 PD 08-FEB-2001.
 PE 28-JUL-2000; 2000WO-JP05060.
 PR 29-JUL-1999; 99JP-0248036.
 PR 18-OCT-1999; 99US-0159590.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 17-FEB-2000; 2000US-0183322.
 PR 02-MAY-2000; 2000JP-0183767.
 PA (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;
 DR WPI: 2001-564736/63.
 DR N-PSDB: AAH78068.
 XX New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes -
 PS Claim 2; Page 125-128; 336pp; Japanese.
 CC The present sequence represents a human protein kinase/protein

phosphatase. The polypeptides are expected to participate in signal
 transduction in cells. The kinase phosphatases are connected with
 intracellular signalling pathways. Antisense oligonucleotides and
 compounds identified by screening (agonists or antagonists) can be
 used to treat human or animal disorders associated with the expression
 or function of the protein. In addition, the polypeptides may be used
 as target molecules for drug development.

Sequence 454 AA;

Query Match 62.9%; Score 1162; DB 22; Length 454;
 Best Local Similarity 64.4%; Pred. No. 4.3e-93;
 Matches 232; Conservative 49; Mismatches 61; Indels 18; Gaps 3;

1 MEPEKQKVEDFYDIDGELSGQFAIVKCKRSTGLTYAAKFIKKRSRARSRCVSRRE 60
 1 mstfrqevdyemgeelsgqfaiivkckrqgkygkeyaakfkkrrlssrrgvsree 60

61 IEREVSIKQVLYHNVTLDHYENRTDVVHILELVSGELFDPFLAQKESLEBEATSPFI 120
 61 Ierevnlirelhpnlitldhdfenktvdllelvsgelldflaekesldeeatqfl 120

121 KQILDGVNVLHTKRIAHFDLKPENIMLDKNIPPIHKLIDFGLAHEIEDGVFNKIFGT 180
 121 kqildgvnylhskriahfdlkipenimldknpnprikliidfglahkieagnefnkifgt 180

181 PEFAVAPEIVNPEPLGLEADMSIGVITYTLLSGASPFGLDQKOEFLANTSVSYDFDEEF 240
 181 pefavapeivnpeplgleadmsigvitytllsgaspfglgelqetclnlsavnydfdeey 240

241 FSHTSELAKDFIRKLIVKETERKRLTIOELRHPWITPVNDQOAWVRRESVNLLENFRKOY 300
 241 fsntgelakdfirllivkdpkrmtlsglseshwl-----kallrrnnvgedsgtkrpe 293

301 VRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDE---DLRNCESDTEEDTARRKALHPRRRS 357
 301 vrrrwklsfslvslcnhltrslmkkvhlrpde---dlrncesdteedtarrkalphrrrs 357

294 rrrlktlrkeytlkskshs-----lppnnsyadferfakvleaaaaeeglrelqrs 345

RESULT 9
 AAY06922
 ID AAY06922 standard; Protein: 448 AA.
 AC AAY06922;
 DT 01-JUL-1999 (first entry)
 DE Murine ZIP-kinase (serine/threonine kinase).
 KW zipper interacting protein kinase; ZIP-kinase; serine/threonine kinase;
 KM leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
 KM human; murine.
 OS Mus musculus.
 PN EP911408-A2.
 PD 28-APR-1999.
 PR 24-SEP-1998; 98EP-0307747.
 PR 26-SEP-1997; 97JP-0261589.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PI Akira S, Kawai T;
 DR WPI: 1999-246420/21.
 DR N-PSDB: AAX34657.
 PT New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase)
 CC protein and DNA, useful as anticancer agents

XX	WP1: 2000-271053/23.
DR	N-PSDB: AA299730, AA299731.
XX	
PT	New nucleic acid encoding cardiovascular system associated protein
PT	kinase, used e.g. for diagnosis, treatment and prevention of
PT	cardiovascular disease
XX	
PS	Claim 2; Fig 4; 163pp; English.
XX	
CC	The present sequence represents a human cardiovascular system associated
CC	protein kinase-4 (CSAPK-4). CSAPK polypeptides are involved in signalling
CC	pathways associated with cell growth and differentiation. The CSAPK
CC	polypeptides and polynucleotides are used to screen for agents that
CC	specifically modulate CSAPK, which are potential therapeutic agents.
CC	They are also used for diagnosis, prognosis or monitoring of
CC	CSAPK-related diseases, gene mapping, tissue typing and forensic
CC	identification, and for treating or preventing disorders associated
CC	with aberrant CSAPK expression or activity, especially cardiovascular
CC	diseases such as congestive heart failure. They can also be used in
CC	pharmacogenomics. The CSAPK polynucleotide may also be used to generate
CC	transgenic animals.
XX	
SO	Sequence 160 AA:
	Query Match 41.2%; Score 761; DB 21; Length 160;
	Best Local Similarity 94.3%; Pred. No. 1,le-58;
	Matches 150; Conservative 4; Mismatches 3; Indels 2; Gaps 1;
OY	202 SIGVTITLLSGASPFLLGDTKQETANTITSYDDEPFHSTSLADFTIKLLYKETR 261
	1: 1:
Db	4 slsyy--lslsgaspfllgdtkqetlanltavsydfdeefsqtselakdfirkllivketr 61
OY	262 KRLTQELRLHPIWIRPVNQAMVRRESVNLNFRKQYRRRMRKLSFSIYSLCNHLTPRS 321
	. 62 krltqealrhpwlrlpvdnqgemvrrsvnlenlrkqyrrrrmrklsfsiyslcnhltrs 121
OY	322 LMKKVLRPDEDLRNCESDTEEDIRARRKALHPRRRSSTS 360
Db	122 lmkvhlrpdedlnrncestdteedlarrrkalhprrrsstts 160
	RESULT 11
ID	AA27161
	AA27161 standard; Protein; 414 AA.
AC	AA27161;
XX	
DT	15-SEP-1999 (first entry)
XX	
DE	Human DRAK1 protein.
KW	DRAK1; DRAK2; DAP kinase related apoptosis inducing kinase; human;
KW	apoptosis; breast cancer; ovarian cancer; lymphoma; autoimmune disease;
KW	viral infection; adenovirus; poxvirus; HIV; Alzheimer's disease;
KW	Parkinson's disease; arteriosclerosis; alcoholism; rheumatoid arthritis;
XX	diabetes.
XX	
OS	Homo sapiens.
XX	
PN	WO9933961-A1.
XX	
PD	08-JUL-1999.
XX	
PF	25-DEC-1998; 98WO-JP05974.
XX	
PR	17-APR-1998; 98JP-0108150.
PR	26-DEC-1997; 97JP-0367640.
PR	26-DEC-1997; 97JP-0367641.
PR	17-APR-1998; 98JP-0108149.
XX	
PA	(ASAH) ASAH KASEI KOGYO KK.


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Query Match 35.8% Score 660; DB 22; Length 7107;
Best Local Similarity 43.2%; Pred. No. 1,1e-47;
Matches 140; Conservative 62; Mismatches 110; Indels 12; Gaps 5

QY      6  QOKVEDFYDIGELSGGFPAIVKCKREKSTGLEVAKFIKKQSRASRGVSHREIEERY 65
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      6131 qgsyvdrydlleeistgfygvhrcrcstgnlfaakffvshs-----vekdrlrrt 6184

QY      66  SLRQVLLHNNTYTLNDYVENKRDVYNHLELVSGGELFD-FLAQKESLSEBATSFTKQI 124
      | : : : : | | | | : : : : | | | | | | | | : : | : : : |
Db      6195 dlmqllhmqklnlndafeddema1lleflsgelferltaeyuymtaevaynmgqic 6244

QY      125 DGVNLFHTKKIAHNPFLKPEEMILLOKNRPIPIKILDFELAHIEEGVGFEKNIFGRPREY 184
      | : : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db      6245 egirmhbnllhldikpenlmqctrs--stcnkllldfslatrlldpnevkklltgcgaeta 6302

QY      185 APEIVNYPEPLGHEADMWSIGVITVYLLSGASPELGDTKQETLANITSVSYDFDEEFSHT 244
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      6303 apelvnrpevgfyctdmwacgvslylllspflagndnqctklknvackwdlfvesfkyI 6362

QY      245 SELANDIRKLKLVKETKRRLTIOEALRNHPWTIPVDN--QOAMVRESVYNLENFKKQYVR 302
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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131 HINAHFDEPENIMLEDKNIFPHIKLIDEGUAHEIEDGVKNIFGIPFVAPELVN 190

Db 115 hkgjivhldkpenimcvnkt--gtsiklidfglarllesagslkvlfgtpefavavein 172

OY 191 YEPFLADAMNSIGVITYILLSGASPFUGDTKQETLANITSVYDFEESHSTSELAND 250
 DB 123 YEPHYGEDMWSIGYICVILVSGISPFMDNDNETLANVTSATWTFIDEAFDEISDADK 232
 OY 251 FTRKLVKETRRLTIOEALRHPWI 275
 DB 233 ftsnllkkkmksrrlncctqlnphwl 257

RESULT 15
 AAB65624
 ID AAB65624 standard; Protein: 372 AA.
 AC AAB65624;
 DT 27-MAR-2001 (first entry)
 DE Novel protein kinase, SEQ ID NO: 150.
 XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
 XX Mus musculus.
 OS
 XX WO200073469-A2.
 PN 07-DEC-2000.
 XX 26-MAY-2000; 2000WO-US14842.
 XX 28-MAY-1999; 99US-0136503.
 PR (SUGEN-) SUGEN INC.
 XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
 PI WPI: 2001-032161/04.
 DR N-PSDB; AAF44650.
 DR
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 PS Claim 10; Fig 1; 310pp; English.
 XX
 CC The present sequence is a novel protein kinase. The novel protein kinases
 CC and the nucleic acids that encode them may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.
 XX
 SQ Sequence 372 AA;

OY 3 PEROKVEDFDYD-GEELSGQFAIVKCKREKSTGLEAYAKFIKKRQSRASRRGV-REE 60
 DB 22 ptktenfnfylltpkelgrgkfavrrgclskstgqyaaksikr-----rrgdcrae 76
 OY 61 IREVSIL--ROYLHNAVITLHDVYENRTDVVHIELVSGGELFDFLAK--ESLSEET 115
 DB 77 lthelavlelarscph--vinlheyenatelllvleayaageifnlclpelaemvsend 134
 OY 116 ATSFTRQIILGVNVLTKKRIAHFDLKPENIMLLDKNIPPIHKLIDPGLAHEIEDGVEFK 175
 DB 135 vlrllkqllegvnylnqnnlvnldlkpqn-llsstypigdkivdfgmsrkignasselr 193
 OY 176 NIFGTPEFVAPETIVNYEPLGLADAMNSIGVITYILLSGASPFUGDTKQETLANITSVSYD 235
 DB 194 elmgpneylapellnydpiltatdmwnlgllymllthscpfvgedngetylnlsqyvnd 253
 OY 236 FDEEFSHTSELANDFIRKLVKETRRLTIOEALRHPWITPYD 279
 DB 254 yseemfssvsglatdfisglvknpekrptaescishswlqgwd 297

Search completed: May 18, 2002, 04:47:24
 Job time: 18478 sec

Query Match 35.2%; Score 649.5; DB 22; Length 372;
 Best Local Similarity 46.8%; Pred. No. 1.8e-48;
 Matches 133; Conservative 52; Mismatches 84; Indels 15; Gaps 7;

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